

WO 01/18047

PCT/AU00/01083

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SEQUENCE LISTING

<110> The Council of the Queensland Institute of Medical Research

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50	Glu	Gly	Ser	Gln	Lys	Asp	Gly	Asn	Phe	Ser	Cys	Gln	Arg	Val	Leu	Phe	
	305					310					315					320	
	Lys	Cys	Lys	Glu	Asp	Val	Ile	Pro	Asp	Asn	Lys	Gln	Ile	Gln	Gln	Cys	
					325					330					335		
55	Gln	Glu	Gly	Thr	Ala	Val	Lys	Pro	Ala	Tyr	Val	Ser	Phe	Cys	Ala	Gln	
				340					345					350			

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	660		665		670
	His Tyr Leu Phe Leu Ala Cys		Phe Phe Trp Met Leu Val Glu Ala Val		
	675		680		685
5	Ile Leu Phe Leu Met Val Arg		Asn Leu Lys Val Val Asn Tyr Phe Ser		
	690		695		700
10	Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu				
	705		710		715
	Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr				
			725		730
					735
15	Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp				
			740		745
					750
	Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu				
			755		760
					765
20	Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn				
			770		775
					780
	Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala				
			785		790
					795
25	Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe				
			805		810
					815
30	Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile				
			820		825
					830
	Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn				
			835		840
					845
35	Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys				
			850		855
					860
	Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro				
			865		870
					875
40	Ser Ala Ser Lys Thr Gly				
			885		
45					
	<210> 6				
	<211> 931				
	<212> PRT				
	<213> Mus musculus				
50					
	<400> 6				
	Met Trp Gly Phe Trp Leu Leu Leu Phe Trp Gly Phe Ser Gly Met Tyr				
	1		5		10
					15
55	Arg Trp Gly Met Thr Thr Leu Pro Thr Leu Gly Gln Thr Leu Gly Gly				
			20		25
					30
	Val Asn Glu Cys Gln Asp Thr Thr Thr Cys Pro Ala Tyr Ala Thr Cys				

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	35	40	45
	Thr Asp Thr Thr Asp Ser Tyr Tyr Cys Thr Cys Lys Arg Gly Phe Leu		
5	50	55	60
	Ser Ser Asn Gly Gln Thr Asn Phe Gln Gly Pro Gly Val Glu Cys Gln		
	65	70	75
10	Asp Val Asn Glu Cys Leu Gln Ser Asp Ser Pro Cys Gly Pro Asn Ser		
	85	90	95
	Val Cys Thr Asn Ile Leu Gly Arg Ala Lys Cys Ser Cys Leu Arg Gly		
	100	105	110
15	Phe Ser Ser Ser Thr Gly Lys Asp Trp Ile Leu Gly Ser Leu Asp Asn		
	115	120	125
	Phe Leu Cys Ala Asp Val Asp Glu Cys Leu Thr Ile Gly Ile Cys Pro		
	130	135	140
20	Lys Tyr Ser Asn Cys Ser Asn Ser Val Gly Ser Tyr Ser Cys Thr Cys		
	145	150	155
	Gln Pro Gly Phe Val Leu Asn Gly Ser Ile Cys Glu Asp Glu Asp Glu		
	165	170	175
25	Cys Val Thr Arg Asp Val Cys Pro Glu His Ala Thr Cys His Asn Thr		
	180	185	190
30	Leu Gly Ser Tyr Tyr Cys Thr Cys Asn Ser Gly Leu Glu Ser Ser Gly		
	195	200	205
	Gly Gly Pro Met Phe Gln Gly Leu Asp Glu Ser Cys Glu Asp Val Asp		
	210	215	220
35	Glu Cys Ser Arg Asn Ser Thr Leu Cys Gly Pro Thr Phe Ile Cys Ile		
	225	230	235
	Asn Thr Leu Gly Ser Tyr Ser Cys Ser Cys Pro Ala Gly Phe Ser Leu		
	245	250	255
40	Pro Thr Phe Gln Ile Leu Gly His Pro Ala Asp Gly Asn Cys Thr Asp		
	260	265	270
45	Ile Asp Glu Cys Asp Asp Thr Cys Pro Leu Asn Ser Ser Cys Thr Asn		
	275	280	285
	Thr Ile Gly Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Ser Ser		
	290	295	300
50	Asn Gly Gln Leu Asn Phe Lys Asp Leu Glu Val Thr Cys Glu Asp Ile		
	305	310	315
	Asp Glu Cys Thr Gln Asp Pro Leu Gln Cys Gly Leu Asn Ser Val Cys		
	325	330	335
55	Thr Asn Val Pro Gly Ser Tyr Ile Cys Gly Cys Leu Pro Asp Phe Gln		
	340	345	350

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	Met	Asp	Pro	Glu	Gly	Ser	Gln	Gly	Tyr	Gly	Asn	Phe	Asn	Cys	Lys	Arg
			355					360					365			
5	Ile	Leu	Phe	Lys	Cys	Lys	Glu	Asp	Leu	Ile	Leu	Gln	Ser	Glu	Gln	Ile
	370						375					380				
	Gln	Gln	Cys	Gln	Ala	Val	Gln	Gly	Arg	Asp	Leu	Gly	Tyr	Ala	Ser	Phe
	385					390					395					400
10	Cys	Thr	Leu	Val	Asn	Ala	Thr	Phe	Thr	Ile	Leu	Asp	Asn	Thr	Cys	Glu
					405					410					415	
	Asn	Lys	Ser	Ala	Pro	Val	Ser	Leu	Gln	Ser	Ala	Ala	Thr	Ser	Val	Ser
15				420					425					430		
	Leu	Val	Leu	Glu	Gln	Ala	Thr	Thr	Trp	Phe	Glu	Leu	Ser	Lys	Glu	Glu
			435					440					445			
20	Thr	Ser	Thr	Leu	Gly	Thr	Ile	Leu	Leu	Glu	Thr	Val	Glu	Ser	Thr	Met
	450						455					460				
	Leu	Ala	Ala	Leu	Leu	Ile	Pro	Ser	Gly	Asn	Ala	Ser	Gln	Met	Ile	Gln
	465					470					475					480
25	Thr	Glu	Tyr	Leu	Asp	Ile	Glu	Ser	Lys	Val	Ile	Asn	Glu	Glu	Cys	Lys
				485						490					495	
	Glu	Asn	Glu	Ser	Ile	Asn	Leu	Ala	Ala	Arg	Gly	Asp	Lys	Met	Asn	Val
30				500					505					510		
	Gly	Cys	Phe	Ile	Ile	Lys	Glu	Ser	Val	Ser	Thr	Gly	Ala	Pro	Gly	Val
			515					520					525			
35	Ala	Phe	Val	Ser	Phe	Ala	His	Met	Glu	Ser	Val	Leu	Asn	Glu	Arg	Phe
	530						535					540				
	Phe	Glu	Asp	Gly	Gln	Ser	Phe	Arg	Lys	Leu	Arg	Met	Asn	Ser	Arg	Val
	545					550					555					560
40	Val	Gly	Gly	Thr	Val	Thr	Gly	Glu	Lys	Lys	Glu	Asp	Phe	Ser	Lys	Pro
				565							570				575	
	Ile	Ile	Tyr	Thr	Leu	Gln	His	Ile	Gln	Pro	Lys	Gln	Lys	Ser	Glu	Arg
45				580					585					590		
	Pro	Ile	Cys	Val	Ser	Trp	Asn	Thr	Asp	Val	Glu	Asp	Gly	Arg	Trp	Thr
			595					600					605			
50	Pro	Ser	Gly	Cys	Glu	Ile	Val	Glu	Ala	Ser	Glu	Thr	His	Thr	Val	Cys
	610						615					620				
	Ser	Cys	Asn	Arg	Met	Ala	Asn	Leu	Ala	Ile	Ile	Met	Ala	Ser	Gly	Glu
	625					630					635					640
55	Leu	Thr	Met	Glu	Phe	Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Thr	Val
					645					650					655	

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Ile Ser Leu Val Cys Leu Ala Leu Ala Ile Ala Thr Phe Leu Leu Cys
 660 665 670
 5 Arg Ala Val Gln Asn His Asn Thr Tyr Met His Leu His Leu Cys Val
 675 680 685
 Cys Leu Phe Leu Ala Lys Ile Leu Phe Leu Thr Gly Ile Asp Lys Thr
 690 695 700
 10 Asp Asn Gln Thr Ala Cys Ala Ile Ile Ala Gly Phe Leu His Tyr Leu
 705 710 715 720
 Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val Met Leu Phe
 725 730 735
 15 Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser Ser Arg Asn
 740 745 750
 Ile Lys Met Leu His Leu Cys Ala Phe Gly Tyr Gly Leu Pro Val Leu
 755 760 765
 20 Val Val Ile Ile Ser Ala Ser Val Gln Pro Arg Gly Tyr Gly Met His
 770 775 780
 25 Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp Ser Phe Leu
 785 790 795 800
 Gly Pro Val Cys Met Ile Ile Thr Ile Asn Ser Val Leu Leu Ala Trp
 805 810 815
 30 Thr Leu Trp Val Leu Arg Gln Lys Leu Cys Ser Val Ser Ser Glu Val
 820 825 830
 Ser Lys Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Ile Ala Gln
 835 840 845
 35 Ile Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly
 850 855 860
 40 Pro Leu Ala Ser Ile Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu
 865 870 875 880
 Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn Arg Gln Val
 885 890 895
 45 Arg Asp Glu Tyr Lys Lys Leu Leu Thr Arg Lys Thr Asp Leu Ser Ser
 900 905 910
 50 His Ser Gln Thr Ser Gly Ile Leu Leu Ser Ser Met Pro Ser Thr Ser
 915 920 925
 Lys Met Gly
 930
 55
 <210> 7
 <211> 740
 <212> PRT

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<213> Homo sapiens

<400> 7

5	Met	Gly	Gly	Arg	Val	Phe	Leu	Ala	Phe	Cys	Val	Trp	Leu	Thr	Leu	Pro
	1				5					10					15	
	Gly	Ala	Glu	Thr	Gln	Asp	Ser	Arg	Gly	Cys	Ala	Arg	Val	Cys	Pro	Gln
			20						25					30		
10	Asn	Ser	Ser	Cys	Val	Asn	Ala	Thr	Ala	Cys	Arg	Cys	Asn	Pro	Gly	Phe
		35						40					45			
	Ser	Ser	Phe	Ser	Glu	Ile	Ile	Thr	Thr	Pro	Thr	Glu	Thr	Cys	Asp	Asp
		50					55					60				
15	Ile	Asn	Glu	Cys	Ala	Thr	Pro	Ser	Lys	Val	Ser	Cys	Gly	Lys	Phe	Ser
	65					70					75					80
	Asp	Cys	Trp	Asn	Thr	Glu	Gly	Ser	Tyr	Asp	Cys	Val	Cys	Ser	Pro	Gly
20					85					90					95	
	Tyr	Glu	Pro	Val	Ser	Gly	Ala	Lys	Thr	Phe	Lys	Asn	Glu	Ser	Glu	Asn
			100						105					110		
25	Thr	Cys	Gln	Asp	Glu	Cys	Ser	Ser	Gly	Gln	His	Gln	Cys	Asp	Ser	Ser
			115					120					125			
	Thr	Val	Cys	Phe	Asn	Thr	Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro
		130					135					140				
30	Gly	Trp	Lys	Pro	Arg	His	Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val
	145					150					155					160
	Cys	Glu	Asp	Met	Thr	Phe	Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His
35					165					170					175	
	Ser	Gln	Thr	Leu	Ser	Arg	Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg
				180					185					190		
40	Asp	Ser	Lys	Thr	Ser	Ser	Ala	Glu	Val	Thr	Ile	Gln	Asn	Val	Ile	Lys
			195					200					205			
	Leu	Val	Asp	Glu	Leu	Met	Glu	Ala	Pro	Gly	Asp	Val	Glu	Ala	Leu	Ala
		210					215					220				
45	Pro	Pro	Val	Arg	His	Leu	Ile	Ala	Thr	Gln	Leu	Leu	Ser	Asn	Leu	Glu
	225					230					235					240
	Asp	Ile	Met	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Pro	Lys	Gly	Pro	Phe	Thr
50					245					250					255	
	Tyr	Ile	Ser	Pro	Ser	Asn	Thr	Glu	Leu	Thr	Leu	Met	Ile	Gln	Glu	Arg
			260					265						270		
55	Gly	Asp	Lys	Asn	Val	Thr	Met	Gly	Gln	Ser	Ser	Ala	Arg	Met	Lys	Leu
			275					280					285			
	Asn	Trp	Ala	Val	Ala	Ala	Gly	Ala	Glu	Asp	Pro	Gly	Pro	Ala	Val	Ala

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290 295 300
Gly Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser
305 310 315 320
5 Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu
325 330 335
10 Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser
340 345 350
Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu
355 360 365
15 Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp
370 375 380
Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys
385 390 395 400
20 Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu
405 410 415
25 Val Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys
420 425 430
Ser His Leu Ser Ser Phe Thr Ile Leu Met Ala His Tyr Asp Val Glu
435 440 445
30 Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu
450 455 460
Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile
465 470 475 480
35 Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe
485 490 495
40 Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln
500 505 510
Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe
515 520 525
45 Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe
530 535 540
Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu
545 550 555 560
50 Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala
565 570 575
Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp
580 585 590
55 Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile
595 600 605

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Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr
 610 615 620
 5 Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala
 625 630 635 640
 Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys
 645 650 655
 10 Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu
 660 665 670
 Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr
 675 680 685
 15 Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys
 690 695 700
 20 Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser
 705 710 715 720
 Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser
 725 730 735
 25 Glu Ser Gly Ile
 740
 30 <210> 8
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 35 <220>
 <223> Description of Artificial Sequence: PCR primers
 <400> 8
 ctacggatcc aatatttcag cttcctgtcc 30
 40
 <210> 9
 <211> 32
 <212> DNA
 45 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: PCR primers
 50 <400> 9
 cgcgaagctt tcaatcttga catttctcat gg 32
 55 <210> 10
 <211> 34
 <212> DNA
 <213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: PCR primers
 <400> 10
 5 gacgggatcc aatgagtgtc tactgaaaga attg 34
 <210> 11
 <211> 34
 10 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: PCR primers
 15 <400> 11
 accgaagctt tcagctcttg ttcacataac aatc 34
 <210> 12
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 25 <220>
 <223> Description of Artificial Sequence: PCR primers
 <400> 12
 30 ctacggatcc aatatttcag ctctctgtcc 30
 <210> 13
 <211> 34
 <212> DNA
 35 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: PCR primers
 40 <400> 13
 accgaagctt tcagctcttg ttcacataac aatc 34
 <210> 14
 45 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 50 <223> Description of Artificial Sequence: PCR primers
 <400> 14
 acacggatcc actttgggag tactgagtga a 31
 55 <210> 15
 <211> 32
 <212> DNA

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<213> Artificial Sequence.

<220>

<223> Description of Artificial Sequence: PCR primers

5

<400> 15

32

cgctaagctt tcatagagcc atgagcacag ca

10

<210> 16

<211> 20

<212> DNA

<213> Mus musculus

15

<400> 16

20

cacctgcagc tcttccatct

20

<210> 17

<211> 23

<212> DNA

<213> Mus musculus

25

<400> 17

23

gaaagtttgc ttctcaaaat cca

30

<210> 18

<211> 26

<212> DNA

<213> Homo sapiens

35

<400> 18

26

tgtctcattg cacctcttgg ttccat

40

<210> 19

<211> 19

<212> DNA

<213> Homo sapiens

45

<400> 19

19

ccacaacagc acccactgt

50

<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

55

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 20

33

tagtagacgc gtatattaca aatgatgaat att

<210> 21

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<211> 33
<212> DNA
<213> Artificial Sequence

5 <220>
<223> Description of Artificial Sequence: PCR primer

<400> 21
tagtagacgc gttcaatcac taatagttct gct 33

10

<210> 22
<211> 26
<212> DNA
15 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

20 <400> 22
cgggatactc ctcattgggt agagcc 26

<210> 23
<211> 33
<212> DNA
25 <213> Artificial Sequence

<220>
30 <223> Description of Artificial Sequence: PCR primer

<400> 23
cgggtaccac catgggaagc aggtgccttc tgc 33

35

<210> 24
<211> 24
<212> DNA
40 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 24
45 ggaaytagaa caccaggttt atca 24

<210> 25
<211> 18
<212> DNA
50 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

55 <400> 25
cctcttctcg gccacac 18